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OM protein - protein search, using sw model.

Run on: December 30, 2002, 16:15:27 ; Search time 29 seconds

(without alignments)
461.830 Million cell updates/sec

Title: us-09-664-326-23
Perfect score: 368
Sequence: 1 LTYNCTESQNCICLCEGSN.....PKPQSHNDGDFEEIPEEYIQ 65

Scoring table: BiOSUM22
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues**Total number of hits satisfying chosen parameters:** 671580**Minimum DB seq length:** 0**Maximum DB seq length:** 200000000**Post-processing:** Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL_21;*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp Rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: spUnclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	247	67.1	84	5 Q07557
2	230	62.5	84	5 Q07558
3	138	37.5	25	5 Q9TWX5
4	136	37.0	25	5 Q9TWX4
5	74.5	20.2	1331	5 Q9W093
6	74	20.1	248	5 Q96962
7	74	20.1	2352	5 Q61240
8	71	19.3	608	5 Q9VU80
9	70	19.0	169	2 Q8RP58
10	70	19.0	323	2 Q93N78
11	69	18.8	315	13 Q9W600
12	68.5	18.6	2233	5 Q94711
13	68	18.5	184	2 Q9RB30
14	68	18.5	278	2 Q9XCP8
15	68	18.5	364	2 Q84968
16	66.5	18.1	181	3 Q96U3

Query Match	67.1%	Score 247; DB 5; Length 84;	OS Hirudinaria manillensis (Buffalo leech), Eukaryote; Metazoa; Annelida; Cliteellata; Hirudinida; Hirudinea;
Best Local Similarity	71.0%	Pred. No. 7.9e-23; Pred. No. 7.9e-23;	OC
Matches	44	Conservative 6; Mismatches 10; Indels 2; Gaps 1;	OC
RESULT 2			OX NCBI_TAXID=6419;
QY 1 LTYDCTESQNLCLCEGSNVCGGNCIGSDSEKNCQSLSSG--NQCVHGETPKPQSQTECDFEIP 60			RN [1]
Db 21 VSYTDCTESQNLCLCVGSNVCGGNCIGSDSEKNCQSLSSG--NQCVHGETPKPQSQTECDFEIP 78			RN RPP SEQUENCE.
QY 61 EE 62			RX MEDLINE-92126909; PubMed-1773002;
Db 79 DE 80			RA Electricwala A., Sawyer R.T., Jones C.P., Atkinson T.;
[1]			RT "Isolation of thrombin inhibitor from the leech Hirudinaria
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-84.			RT manillensis.",
RX MEDLINE-9285156; PubMed-768281;			RL Blood Coagul. Fibrinolysis 2:83-89(1991).
RA Scacheri B., Nitti G., Valsasina B., Orsini G., Visco C., Ferrera M.,			DR HSSP; P01050; IHC.
RA Sawyer R.T., Sarmiento P.;			DR InterPro; IPR00429; Hirudin.
RT "Novel hirudin variants from the leech Hirudinaria manillensis. Amino acid sequence, cDNA cloning and genomic organization.";			DR Pfam; PF00713; Hirudin, 1..
RL Eur. J. Biochem. 214:295-304(1993).			DR PRINS; PR00777; HIRUDIN.
CC -1. FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE			FT NON_TER 1 1
CC INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-			FT NON_TER 25 25
CC THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINOGEN.			FT NON_TER 25 AA; 2596 MW; 5296369273A9457D CRC64;
CC -1. SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.			FT NON_TER 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
EMBL; X72785; CA35292.1; -.			QY 1 LTYDCTESQNLCLCEGSNVCGG 25
DR HSSP; P01050; SHIR.			Db 1 LTYDCTESQNLCLCEGSNVCGG 25
DR InterPro; IPR00429; Hirudin.			
DR Pfam; PF00713; Hirudin, 1.			
DR PRINTS; PR00777; HIRUDIN.			
DR ProDom; P004216; Hirudin, 1.			
KW Serine Protease inhibitor; Multigene family; Signal.			
FT SIGNAL 1 20			
FT CHAIN 21 84			
FT DISULFID 25 34			
FT DISULFID 36 48			
FT DISULFID 42 57			
SQ SEQUENC 84 AA; 8934 MW; 3AD73ETD2D4CID CRC64;			
Query Match	62.5%	Score 230; DB 5; Length 84;	OS Hirudinaria manillensis (Buffalo leech), Eukaryote; Metazoa; Annelida; Cliteellata; Hirudinida; Hirudinea;
Best Local Similarity	64.5%	Pred. No. 9.5e-21; Indels 2; Gaps 1;	OC
Matches	40	Conservative 8; Mismatches 12; Indels 2; Gaps 1;	OC
RESULT 3			OX NCBI_TAXID=6419;
Q9TWX5 PRELIMINARY; PRT; 25 AA.			RN RPP SEQUENCE.
Q9TWX5			RX MEDLINE-92126909; PubMed-1773002;
AC			RA Electricwala A., Sawyer R.T., Jones C.P., Atkinson T.;
Q9TWX5; 01-MAY-2000 (TREMBLrel. 13, Created)			RT "Isolation of thrombin inhibitor from the leech Hirudinaria
DT 01-JUN-2002 (TREMBLrel. 13, Last sequence update)			RT manillensis.",
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			RL Blood Coagul. Fibrinolysis 2:83-89(1991).
DE Hirudin variant HV2-THROMBIN inhibitor (Fragment).			DR HSSP; P01050; IHC.
DE Hirudin variant HV2-THROMBIN inhibitor (Fragment).			DR InterPro; IPR00429; Hirudin.
DE Hirudin variant HV2-THROMBIN inhibitor (Fragment).			DR Pfam; PF00713; Hirudin, 1..
DE Hirudin variant HV2-THROMBIN inhibitor (Fragment).			DR PRINS; PR00777; HIRUDIN.
RESULT 4			FT NON_TER 1 1
Q9TWX4 PRELIMINARY; PRT; 25 AA.			FT NON_TER 25 AA; 2596 MW; 5296369273A9457D CRC64;
Q9TWX4			FT NON_TER 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
AC			QY 1 LTYDCTESQNLCLCEGSNVCGG 25
Q9TWX4; 01-MAY-2000 (TREMBLrel. 13, Created)			Db 1 LTYDCTESQNLCLCEGSNVCGG 25
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE Hirudin variant HV2-THROMBIN inhibitor (Fragment).			
OS Hirudinaria manillensis (Buffalo leech), Eukaryote; Metazoa; Annelida; Cliteellata; Hirudinida; Hirudinea;			
OC Arynobdellida; Hirudiniformes; Hirudinidae; Hirudinaria.			
OX NCBI_TAXID=6419;			
RN RPP SEQUENCE.			
RX MEDLINE-92126909; PubMed-1773002;			
RA Electricwala A., Sawyer R.T., Jones C.P., Atkinson T.;			
RT "Isolation of thrombin inhibitor from the leech Hirudinaria			
RT manillensis.",			
RL Blood Coagul. Fibrinolysis 2:83-89(1991).			
DR HSSP; P01050; IHC.			
DR InterPro; IPR00429; Hirudin.			
DR Pfam; PF00713; Hirudin, 1..			
DR PRINS; PR00777; HIRUDIN.			
FT NON_TER 1 1			
FT NON_TER 25 25			
FT SEQUENCE 25 AA; 2580 MW; BC50A99273A9457E CRC64;			
Query Match	37.0%	Score 136; DB 5; Length 25;	OS Hirudinaria manillensis (Buffalo leech), Eukaryote; Metazoa; Annelida; Cliteellata; Hirudinida; Hirudinea;
Best Local Similarity	92.0%	Pred. No. 8.2e-10; Indels 0; Gaps 0;	OC
Matches	23	Conservative 1; Mismatches 1; Indels 0; Gaps 0;	OC
RESULT 5			OX NCBI_TAXID=6419;
Q90W93 PRELIMINARY; PRT; 1331 AA.			RN RPP SEQUENCE.
Q90W93			RX MEDLINE-92126909; PubMed-1773002;
AC			RA Electricwala A., Sawyer R.T., Jones C.P., Atkinson T.;
Q90W93; 01-DEC-2001 (TREMBLrel. 19, Created)			RT "Isolation of thrombin inhibitor from the leech Hirudinaria
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			RT manillensis.",
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			RL Blood Coagul. Fibrinolysis 2:83-89(1991).
DE Xanthine dehydrogenase.			DR HSSP; P01050; IHC.
DE Poecilia reticulata (Guppy).			DR InterPro; IPR00429; Hirudin.
DE Poecilia reticulata (Guppy).			DR Pfam; PF00713; Hirudin, 1..
DE Poecilia reticulata (Guppy).			DR PRINS; PR00777; HIRUDIN.
DE Poecilia reticulata (Guppy).			FT NON_TER 1 1
DE Poecilia reticulata (Guppy).			FT NON_TER 25 AA; 2596 MW; 5296369273A9457D CRC64;
DE Poecilia reticulata (Guppy).			FT NON_TER 23; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DE Poecilia reticulata (Guppy).			QY 1 LTYDCTESQNLCLCEGSNVCGG 25
DE Poecilia reticulata (Guppy).			Db 1 LTYDCTESQNLCLCEGSNVCGG 25
DE Poecilia reticulata (Guppy).			

Qy	57	EELPEEY	63
Db	203	VDFPREY	209
RN		SEQUENCE FROM N.A. TISSUE-CAUDAL FIN; RA Ben J., Lim T.-M., Chan W.-K., Phang V.P.E.; RT "Molecular cloning of xanthine dehydrogenase gene from guppy (Poecilia reticulata)." ; RL Submitted (May-2001) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AY034103; AAK59599.1; -;	InterPro; IPR02888; ZFE_2S_ferredoxin.	
DR	InterPro; IPR00564; Aldan_dh_C	InterPro; IPR005107; Co-deh_flav_C.	
DR	InterPro; IPR02446; dehydrod_molyb.	InterPro; IPR00572; Euk_Mb_oxid.	
DR	InterPro; IPR01051; Ferredoxin.	InterPro; IPR01315; Ald_xan_dh_C; 1.	
DR	Pfam; PF02738; Ald_xan_dh_C2; 1.	Pfam; PF03450; Co-deh_flav_C; 1.	
DR	Pfam; PF00941; FAD_bihgning_5; 1.	Pfam; PF00111; fer2; 1.	
DR	Pfam; PF01799; fer2_2; 1.	Pfam; PF016071; 2FEE_2S_bind; 1.	
DR	PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.	PROSITE; PS00559; MOLYBDOPTERIN_EUR; UNKNOWN_1.	
KW	Iron-sulfur;	SEQUENCE 1331 AA; 146336 MW; E88EE00AA6D36D126 CRC64;	
SO		Query Match Best Local Similarity 32.2%; Pred. No. 2; Matches 19; Conservative 7; Mismatches 22; Indels 11; Gaps 3;	
Qy	2	TWYDCTES-GQNCLCCEG-----SNVCGQGNKCLIGSDGEKRKNQCVTGEGTPKPQSH 51	
Db	138	TMDITDQALGGNLCRGTGYRPTIVDGCRTRFCQEGNC--QANGGADCLNGEQTNESEH 194	
RESULT 6			
ID	096962	PRELIMINARY; PRT; 248 AA.	
AC	096962;		
DT	01-MAY-1999 (TREMBlrel. 10, Created)		
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)		
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)		
DE	Tetraspanin-CD63 receptor.		
GN	CD63R.		
OS	Suberites domuncula (Sponge).		
OC	Eukaryota; Metazoa; Porifera; Demospongidae; Tetractinomorpha;		
OC	Hadromerida; Suberitidae; Suberites.		
OX	NCBI_TaxID-55567;		
[1]		SEQUENCE FROM N.A.	
RA	Muelner W.E.G., Schatton W., Wimmer W., Bohn M., Batel R., Filic Z.;		
RT	Initiation of an aquaculture of sponges for their sustainable production of biactive metabolites in open systems.";		
RL	Mol. Mar. Biolog. Biotechnol. 1:569-579(1999).		
DR	EMBL; Y18100; CAA77026_1; -.	InterPro; IPR000301; transmembrane_4.	
DR	Pfam; PF00325; transmembrane_4; 1.	Pfam; PR00259; TMFOUR.	
KW	Receptor.		
SO		SEQUENCE 248 AA; 26701 MW; DB0F8D349A2E6EE CRC64;	
Query Match Best Local Similarity 20.1%; Score 74; DB 5; Length 248; Matches 20; Conservative 4; Mismatches 18; Indels 18; Gaps 4;			
Qy	2	TWYDCTES-GQNCLCCEG-----SNVCGQGNKCLIGSDGEKRKNQCVTGEGTPKPQSH 45	
Db	977	TGHC-BEIQN-DCTGENICKNGSCQTNTVSCNCILGGYEST 1018	
RESULT 8			
ID	097080	PRELIMINARY; PRT; 608 AA.	
AC	097080;		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)		
DE	CG10089 protein.		
GN	CG10089.		
OS	Drosophila melanogaster (Fruit fly).		

		Best Local Similarity 39.5%; Pred. No. 19; Matches 17; Conservative 4; Mismatches 13; Indels 9; Gaps 3;	
RESULT 11			
ID Q9W600	PRELIMINARY;	PRT; 315 AA.	
AC Q9W600;			
DT 01-NOV-1999 (TREMBrel. 12, Created)			
DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)			
DE 01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DE Fltk protein.			
GN FLIK.			
OS Gallus gallus (Chicken).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Archosauria; Aveo; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC Gallus.			
NCBI_TaxID=9031;			
[1]			
SEQUENCE FROM N.A.			
RA Patel K;			
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=96427388; PubMed=8812133;			
RA Patel K., Connolly D., Amthor H., Nose K.;			
RT "Cloning and early dorsal-axial expression of Fltk, a chick follistatin-related gene: Evidence for involvement in dorsalisation/neural induction.";			
RL Dev. Biol. 178:37-342(1996).			
DR EMBL; Au238977; CAB42968.1; -.			
DR InterPro; IPR020208; EF-hand.			
DR InterPro; IPR03655; F01N.			
DR InterPro; IPR02355; kazal.			
DR Pfam; PF00050; kazal; 1.			
DR SMART; SM00274; F01N; 1.			
DR SMART; SM00280; KAZAL; 1.			
DR SEQUENCE 315 AA; 35815 MW; C01889B005658A67 CRC64;			
Query Match, 18.8%; Score 69; DB 13; Length 315; Best Local Similarity 33.3%; Pred. No. 2; Mismatches 6; Indels 21; Gaps 3; Matches 21; Conservative 6; RT			
QY 7 TEGCGONLICG-----EGSNVCCQGNKCTLG-SDGKEKNQCVNGEGTPKQPSHNDGFREI 59			
Db 45 TEKGEPCTLCIECKBCKPHGRPVCCNSNGKTYLNHCELHRDACLGS--KIQVDGDHEKEK 101			
QY 60 PEB 62			
Db 102 KSE 104			
RESULT 12			
ID Q94711	PRELIMINARY;	PRT; 2233 AA.	
AC Q94711;			
DT 01-FEB-1997 (TREMBrel. 02, Created)			
DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)			
DE 01-DEC-2001 (TREMBrel. 19, Last annotation update)			
OS SIC1 surface protein.			
OC Paramecium tetraurelia.			
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida; NCBI_TaxID=5888;			
OX [1]			
RP SEQUENCE FROM N.A. MEDLINE=92106337; PubMed=1762150;			
RA Nielsen E., You Y., Forney J.;			
RT variable surface proteins from Paramecium tetraurelia.";			
RL Mol. Biol. 222:835-841(1991).			
DR EMBL; MG5164; AAC01401; -.			
DR InterPro; IPR002855; Paramecium_SA.			
DR Pfam; PF01508; Paramecium_SA; 25.			
DR SEQUENCE 2233 AA; 237078 MW; C064FHOAFTBB873B CRC64;			
Query Match, 18.6%; Score 68.5; DB 5; Length 2233; RT			
RESULT 13			
ID Q9RB30	PRELIMINARY;	PRT; 184 AA.	
AC Q9RB30;			
DT 01-MAY-2000 (TREMBrel. 13, Created)			
DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)			
DE 44 kDa major outer membrane protein (Fragment).			
GN P44-15.			
OS Anaplasma phagocytophylum (Ehrlichia phagocytophila).			
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC Anaplastmataceae; Anaplasma.			
OX NCBI_TaxID=948;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=HZ;			
RX MEDLINE=99292751; PubMed=10364227;			
RA Zhi N., Ohashi N., Rikitisa Y.;			
RT "Multiple p44 genes encoding major outer membrane proteins are expressed in the human granulocytic ehrlichiosis agent.";			
RL J. Biol. Chem. 274:17828-17836(1999).			
DR EMBL; AF132651; AAC01485.1; -.			
DR InterPro; IPR02556; Surface_Ag_msp4.			
DR Pfam; PF01617; Surface_Ag_2; 1.			
FT NON_TER 1			
FT NON_TER 184 AA; 19245 MW; 2BC9AD4775FD55A1 CRC64;			
SQ SEQUENCE 184 AA; 19245 MW; 2BC9AD4775FD55A1 CRC64;			
Query Match, 18.5%; Score 68; DB 2; Length 184; Best Local Similarity 29.6%; Pred. No. 1.5; Mismatches 6; Indels 10; Gaps 3; Matches 21; Conservative 10; RT			
QY 6 CTESGONLICLCEGSNVCCQGN-----KCLIGSDGEKN-QCVNGEGTPKQPSHNDGF- 56			
Db 77 CGDNGSSTTNTSGANSETGQVERDFIRATLKEDGSKNWPTSSGTGPKPVTDNAKWA 136			
QY 57 -----EEIFPEE 62			
Db 137 KDLVQELTPPEE 147			
RESULT 14			
ID Q9XCP8	PRELIMINARY;	PRT; 278 AA.	
AC Q9XCP8;			
DT 01-NOV-1999 (TREMBrel. 12, Created)			
DT 01-NOV-1999 (TREMBrel. 12, Last sequence update)			
DE 01-JUN-2002 (TREMBrel. 21, Last annotation update)			
DE 44 kDa major outer membrane protein (Fragment).			
GN P44-15.			
OS Anaplasma phagocytophylum (Ehrlichia phagocytophila).			
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;			
OC Anaplastmataceae; Anaplasma.			
OX NCBI_TaxID=948;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=HZ;			
RX MEDLINE=99292751; PubMed=10364227;			
RA Zhi N., Ohashi N., Rikitisa Y.;			
RT "Multiple p44 genes encoding major outer membrane proteins are expressed in the human granulocytic ehrlichiosis agent.";			
RL J. Biol. Chem. 274:17828-17836(1999).			
DR EMBL; AF132651; AAC01485.1; -.			
DR InterPro; IPR02556; Surface_Ag_msp4.			
DR Pfam; PF01617; Surface_Ag_2; 1.			

FT NON_TER 1 1
 SQ 278 AA; 29389 MW; BD5B539BB3AE16C7 CRC64;
 Query Match 18.5%; Score 68; DB 2; Length 278;
 Best Local Similarity 29.6%; Pred. No. 2.3;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;
 QY 6 CTESQNLCLCEGSWVGQGN-----KCTIGSGEKN-QCVTGEGTPKPQSHNDGDF-- 56
 Db 120 CGDGSSTINSGANVSETGQVFRDFIRATLKDGSKNWPTSSGTTGTPKPVTNDNAKAVA 179
 QY 57 ---EEIPEE 62
 Db 180 KDLVQELTPEE 190

RESULT 15.

084968 PRELIMINARY; PRT; 364 AA.
 ID 084968
 AC 084968;
 DT 01-NOV-1998 (T-EMBL; 08, Created)
 DT 01-NOV-1998 (T-EMBL; 08, last sequence update)
 DE Major surface protein-2C.
 GN MSP-2C.
 OS Anaplasma phagocytophylum (Ehrlichia Phagocytophilia).
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Anaplasmataceae; Anaplasma.
 OX NCBI_TaxID=948;
 RN [1]
 RP STRAIN=US3;
 RX MEDLINE=98339872; PUBMED=9672253;
 RA Murphy C.I., Storey J.R., Recchia J., Doros-Richert L.A.,
 Gingrich-Baker C., Munroe K., Bakken J.S., Coughlin R.T., Beltz G.A.;
 RT "Major antigenic proteins of the agent of human granulocytic
 ehrlichiosis are encoded by members of a multigene family.",
 RL Infect. Immun. 66:3711-3718(1998).
 DR EMBL; AF029323; AAC31309 1;
 DR InterPro; IPR002566; Surface_Ag_msp4.
 DR Pfam; PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 364 AA; 38805 MW; 32D9B830A6153F2 CRC64;
 Query Match 18.5%; Score 68; DB 2; Length 364;
 Best Local Similarity 29.6%; Pred. No. 3.1;
 Matches 21; Conservative 10; Mismatches 26; Indels 14; Gaps 3;
 QY 6 CTESQNLCLCEGSWVGQGN-----KCTIGSGEKN-QCVTGEGTPKPQSHNDGDF-- 56
 Db 226 CGDGSSTINSGANVSETGQVFRDFIRATLKDGSKNWPTSSGTTGTPKPVTNDNAKAVA 285
 QY 57 ---EEIPEE 62
 Db 286 KDLVQELTPEE 296

Search completed: December 30, 2002, 16:17:37
 Job time : 31 secs